

TITLE: ANALYSIS OF FIVE NEAR COMPLETE GENOME SEQUENCES FOR MEMBERS OF THE PHYLUM THAUMARCHAEOTA FROM THE AMAZON RIVER AND PLUME

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ABSTRACT:

The Amazon River is considered the world's largest riverine system. It carries a huge amount of organic matter and nutrients to the oceans, thus contributing to nutrient cycling at global scale. Moreover, tropical freshwater environments are important reservoirs of microbial life. Previous studies have demonstrated the presence of Thaumarchaeota in the Amazon River. This prokaryote group is well known as important contributors to C and N cycles. Despite its importance the role of this group in the Amazon River is still underexplored. The main aim of this study was to recover Thaumarchaeota genomes from metagenomic data obtained from de Amazon Plume and River. In order to achieve this goal, sequences obtained with Illumina HiSeq platform were previously assembled. Binning of assembled scaffolds was performed based on GC content, coverage and taxonomy assignment using de pipeline ggkbase (UC Berkeley). Taxonomic analysis revealed that Thaumarchaeota were one of the most abundant microbial groups in the river comprising 10.85%, which indicate that this group may play an important role in this freshwater environment. We recovered five near complete genomes for members of the phylum Thaumarchaeota. The genome size varied from 943 Kbp to 2.16 Mbp and the GC content varied from 33% to 38%. The genome analysis revealed the presence of genes encoding for ammonia monooxygenase and nitrate reductase, important enzymes for the N cycle. Archaea are frequently reported as ammonia oxidizing. Furthermore, genes related to urea metabolism were also present. It has been demonstrated that urea may play a role in marine nitrification by Thaumarchaeota. Metabolism of urea to CO₂ and ammonia can subsequently feed carbon fixation and ammonia oxidation pathways. Utilization of urea therefore could represent an important source of N for nitrification. Genes related to methane oxidation were also reported. Methane is an important greenhouse gas. Therefore, suggesting that the Thaumarchaeota also may play an important role in the balance between production and oxidation of methane in this riverine environment. The genomes reported here provide new insights into the ecology of this important group of aquatic microbes in the Amazon River and plume

Keywords: Amazon River, metagenome, genome, Thaumarchaeota

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